SEQUENCE LISTING

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<110> COEN, LAURENT
      PINZOLAS, ROSARIO OSTA
      BRULET, PHILIPPE

<120> HYBRID PROTEINS THAT MIGRATE RETROGRADELY AND
      TRANSYNAPTICALLY INTO THE CNS

<130> 03495.0174-01000

<140> 09/816,467
<141> 2001-03-26

<150> 60/055,615
<151> 1997-08-14

<150> 60/065,236
<151> 1997-11-13

<160> 19

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Clostridium tetani

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<221> CDS
<222> (88)..(1476)

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aagctggagc tcggtacccg ggccacc atg gtt ttt tca aca cca att cca ttt 114
                              Met Val Phe Ser Thr Pro Ile Pro Phe
                               1               5

tct tat tct aaa aat ctg gat tgt tgg gtt gat aat gaa gaa gat ata   162
Ser Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile
 10                  15                  20                  25

gat gtt ata tta aaa aag agt aca att tta aat tta gat att aat aat   210
Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn
                 30                  35                  40

gat att ata tca gat ata tct ggg ttt aat tca tct gta ata aca tat   258
Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr
             45                  50                  55

cca gat gct caa ttg gtg ccc gga ata aat ggc aaa gca ata cat tta   306
Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu
         60                  65                  70
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gta aac aat gaa tct tct gaa gtt ata gtg cat aaa gct atg gat att   354
Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile
     75                  80                  85

gaa tat aat gat atg ttt aat aat ttt acc gtt agc ttt tgg ttg agg   402
Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
 90                  95                 100                 105

gtt cct aaa gta tct gct agt cat tta gaa caa tat ggc aca aat gag   450
Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu
                110                 115                 120

tat tca ata att agc tct atg aaa aaa cat agt cta tca ata gga tct   498
Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser
            125                 130                 135

ggt tgg agt gta tca ctt aaa ggt aat aac tta ata tgg act tta aaa   546
Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys
        140                 145                 150

gat tcc gcg gga gaa gtt aga caa ata act ttt agg gat tta cct gat   594
Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp
    155                 160                 165

aaa ttt aat gct tat tta gca aat aaa tgg gtt ttt ata act att act   642
Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr
170                 175                 180                 185

aat gat aga tta tct tct gct aat ttg tat ata aat gga gta ctt atg   690
Asn Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met
                190                 195                 200

gga agt gca gaa att act ggt tta gga gct att aga gag gat aat aat   738
Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn
            205                 210                 215

ata aca tta aaa cta gat aga tgt aat aat aat aat caa tac gtt tct   786
Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser
        220                 225                 230

att gat aaa ttt agg ata ttt tgc aaa gca tta aat cca aaa gag att   834
Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile
    235                 240                 245

gaa aaa tta tac aca agt tat tta tct ata acc ttt tta aga gac ttc   882
Glu Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe
250                 255                 260                 265

tgg gga aac cct tta cga tat gat aca gaa tat tat tta ata cca gta   930
Trp Gly Asn Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val
                270                 275                 280

gct tct agt tct aaa gat gtt caa ttg aaa aat ata aca gat tat atg   978
Ala Ser Ser Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met
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tat ttg aca aat gcg cca tcg tat act aac gga aaa ttg aat ata tat   1026
Tyr Leu Thr Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr
        300                 305                 310

tat aga agg tta tat aat gga cta aaa ttt att ata aaa aga tat aca   1074
Tyr Arg Arg Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr
    315                 320                 325

cct aat aat gaa ata gat tct ttt gtt aaa tca ggt gat ttt att aaa   1122
Pro Asn Asn Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys
330                 335                 340                 345

tta tat gta tca tat aac aat aat gag cac att gta ggt tat ccg aaa   1170
Leu Tyr Val Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys
                350                 355                 360

gat gga aat gcc ttt aat aat ctt gat aga att cta aga gta ggt tat   1218
Asp Gly Asn Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr
            365                 370                 375

aat gcc cca ggt atc cct ctt tat aaa aaa atg gaa gca gta aaa ttg   1266
Asn Ala Pro Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu
        380                 385                 390

cgt gat tta aaa acc tat tct gta caa ctt aaa tta tat gat gat aaa   1314
Arg Asp Leu Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys
    395                 400                 405

aat gca tct tta gga cta gta ggt acc cat aat ggt caa ata ggc aac   1362
Asn Ala Ser Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn
410                 415                 420                 425

gat cca aat agg gat ata tta att gca agc aac tgg tac ttt aat cat   1410
Asp Pro Asn Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His
                430                 435                 440

tta aaa gat aaa att tta gga tgt gat tgg tac ttt gta cct aca gat   1458
Leu Lys Asp Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp
            445                 450                 455

gag gga tgg aca aat gat taaacagatt gatatgttca tgacatatgc          1506
Glu Gly Trp Thr Asn Asp
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<213> Clostridium tetani

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Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser
35 40 45

Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro
50 55 60

Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu
65 70 75 80

Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn
85 90 95

Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser
100 105 110

His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met
115 120 125

Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys
130 135 140

Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg
145 150 155 160

Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala
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Asn Lys Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala
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Asn Leu Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly
195 200 205

Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg
210 215 220

Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe
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Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr
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Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr
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Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val
275 280 285

Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser
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Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly
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Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser
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Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn Asn
340 345 350

Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe Asn Asn
355 360 365

Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile Pro Leu
370 375 380

Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu Lys Thr Tyr Ser
385 390 395 400

Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser Leu Gly Leu Val
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Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn Arg Asp Ile Leu
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ggtcaaatag gcaacgatcc aaatagggat atattaattg caagcaactg gtactttaat 1320
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acaaatgatt aa 1392

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<211> 18
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<220>
<223> Description of Artificial Sequence: Primer

<400> 5
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<210> 6
<211> 25
<212> DNA
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<220>
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<210> 9
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<212> DNA
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<210> 19
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